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Curriculum Vitae

Education

- 2003–2008 Ph.D. in Mathematics (with distinction), Institute of Mathematics, Polish Academy of Sciences
- 1998–2003 M.Sc. in Computer Science, Warsaw University, Interfaculty Individual Studies in Mathematical and Natural Sciences.

Professional experience

- 2011- VIII 2011 Assistant professor at the Institute of Informatics, University of Warsaw
Short fellowship at the Kavli Institute for Theoretical Physics in Santa Barbara, USA
- 2008-2011 Post-doctoral fellowship at the European Molecular Laboratory in Heidelberg, Germany
- X 2003–2008 Teaching Assistant at the Faculty of Mathematics, Mechanics and Informatics, Warsaw University.
- X 2002– VI 2003 Research scholarship at *Lawrence Livermore National Laboratory*, Livermore, USA.

Awards

- 2015 University of Warsaw Rector's awards for organizational achievement
- 2013-2015 Ministry of Science Scholarship for outstanding young scientists
- 2012-2016 EMBO Installation grant
- 2012 Skills-INTER Award of the FNP foundation
- 2012 University of Warsaw Rector's awards for scientific achievement
- 2007-2008 START Fellowship of the FNP foundation

Selected publications

- 2017
- Taking promoters out of enhancers in sequence based predictions of tissue-specific mammalian enhancers, Julia Herman-Izycka, Michal Wlasnowolski and Bartek Wilczynski, *BMC Medical Genomics (Suppl 1)*:34, 2017, DOI: 10.1186/s12920-017-0264-3
- 2016
- Arabidopsis SWI/SNF chromatin remodeling complex binds both promoters and terminators to regulate gene expression, Archacki, R., Yatusевич, R., Buszewicz, D., Krzyczmonik, K., Patryn, J., Iwanicka-Nowicka, R., Biecek, P., Wilczynski, B., Koblowska, M., Jerzmanowski, A., *Nucleic Acids Research*, gkw1273,
- 2015
- Optimally choosing PWM motif databases and sequence scanning approaches based on ChIP-seq data, M Dabrowski, N Dojer, I Krystkowiak, B Kaminska, B Wilczynski, *BMC bioinformatics* 16 (1), 140
 - RECORD: reference-assisted genome assembly for closely related genomes, K. Buza, B. Wilczynski, N. Dojer, *International Journal of Genomics*, Volume 2015, Article ID 563482

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- 2014
- Supervised learning method for predicting chromatin boundary associated insulator elements, P Bednarz, B Wilczyński, *Journal of bioinformatics and computational biology* 12 (06)
- 2013
- Active enhancer positions can be accurately predicted from chromatin marks and collective sequence motif data, A Podsiadło, M Wrzesień, W Paja, W Rudnicki, B Wilczyński, *BMC Systems Biology*, 7, (Suppl. 6), S16
- 2012
- Predicting spatial and temporal gene expression using an integrative model of transcription factor occupancy and chromatin state, B. Wilczynski, YH.Liu, ZX.Yeo, EEM Furlong, *PLoS Computational Biology*, 2012. featured in *Nat. Rev. Genetics*
 - Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development, S. Bonn, R.P. Zinzen, C. Girardot, E.H. Gustafson, A. Perez-Gonzalez, N. Delhomme, Y. Ghavi-Helm, B. Wilczyński, A. Riddell, EEM. Furlong, *Nature Genetics*, Volume 44, Number 2, pages 148–156, 2012, doi:10.1038/ng.1064
- 2010
- Dynamic CRM occupancy reflects a temporal map of developmental progression, Bartek Wilczynski, Eileen EM Furlong, *Molecular Systems Biology* 6 Article number: 383 doi:10.1038/msb.2010.35
- 2009
- Finding evolutionarily conserved cis-regulatory modules with a universal set of motifs, Bartek Wilczynski, Norbert Dojer, Mateusz Patelak and Jerzy Tiuryn, *BMC Bioinformatics* 2009 DOI: 10.1186/1471-2105-10-82
- 2006
- Applying Dynamic Bayesian Networks to Perturbed Gene Expression Data, *Norbert Dojer, Anna Gambin, Bartek Wilczyński, Jerzy Tiuryn*, *BMC Bioinformatics*, 2006, 7:249.
- 2005
- Discovering regulatory binding site modules using rule-based learning, *T.R. Hvidsten, B. Wilczyński, A. Kryshafovich, J. Komorowski and K. Fidelis*, *Genome Research*, 15:856-866, 2005.